IN THE SPECIFICATION:

Please amend the Specification as follows:

At page 13, in the paragraph beginning with "Figure 1" please amend as follows:

Figure 1 illustrates an amino acid sequence alignment of archaeal family B DNA polymerases, corresponding to residues 1-130 of *Pyrococcus furiosus* polymerase. Candidates were identified using a WUBLAST search (European Bioinformatics Institute, http://www.ebi.ac.uk/ebi_home.html) for homologues of Pfu-Pol. An additional ENTREZ search of the SWISSPROT database for family B DNA polymerises polymerases was performed [[[]](Genbank, [[()]http://www.ncbi.nlm.nih.gov/)[[]]]. Sequence alignments were generated using ClustalX (version 1.81) [J. D. Thompson *et al.*, *Nucl. Acids. Res* 24, 4876 (1997)]. The organisms and the DNA polymerase sequence accession numbers were: *Pyrococcus furiosus* (Pfu) (SEQ ID NO: 18) (P80061), *Thermococcus gorgonarius* (Tgo) (SEQ ID NO: 19) (pdb 1D5A), *Pyrococcus kodakaraensis* (PKOD) (SEQ ID NO: 20) (gi/13399597), *Desulfurococcus* strain Tok (DTok) (SEQ ID NO: 21), *Thermococcus sp.* 9°N-7 (9°N-7) (SEQ ID NO: 22) (Q56366), *Thermococcus litoralis* (Tli) (SEQ ID NO: 23) (AAA72101.1), *Methanococcus voltae* (Mvo) (SEQ ID NO: 24) (P52025), *Pyrobaculum islandicum* (Pis) (SEQ ID NO: 25) (AAF27815.1), *Archaeoglobus fulgidus* (A[[g]]fu) (SEQ ID NO: 26) (O29753), *Cenarchaeaum symbiosum* (Csy) (SEQ ID NO: 27) (AAC62712.1), *Sulfolobus acidocaldarius* (Sac) (SEQ ID NO: 28) (P95690), *Sulfurisphaera ohwakuensis* (Soh) (SEQ ID NO: 29) (BAA23994.1), *Sulfolobus solfataricus* (Sso) (SEQ ID NO: 30) (P26811), *Pyrodictium occultum* (Poc) (SEQ ID NO: 31) (BAA07579.1) and *Aeropyrum pernix* (Ape) (SEQ ID NO: 32) (NP_148473.1)[[;]].

At page 13, in the paragraph beginning with "Figure 2A" and bridging pages 13 and 14, please amend as follows:

Figure 2A: The template-binding cleft T (21) of Tgo-Pol showing the presence of a pocket. B: The N-terminal domain of Tgo-Pol (SEQ ID NO:12) with amino acids that form the

pocket shown in space-fill: Y7; P36/Y37; amino acids 90-97 (22); amino acids 112-116 (23). α-Helices are shown (24) and β-sheets (25). C: Amino acid sequences of the N-terminal domains of Tgo-Pol (upper sequence (SEQ ID NO.12)) and RB69-Pol (lower sequence (SEQ ID NO.13)). Amino acids that form the pocket in Tgo-Pol (and the corresponding residues in RB69-Pol) are underlined and correspond to the amino acids identified in panels B and E. Cylinders represent α-helices and arrows β-sheets. The amino acid sequences have minimal homology and have been aligned using structural homology. D: Structural alignment of the N-terminal domains of Tgo-Pol (SEQ ID NO:12) and RB69-Pol (SEQ ID NO:13). The insert in Tgo-Pol is shown (26). This structural superimposition was used to generate the amino acid alignment shown in C. E: The N-terminal domain of RB69-Pol (SEQ ID NO:13). Space-filled amino acids (V8 Q10; residues 65-72 (27); residues 84-89 (28); P35/S36 lie substantially behind residues 84-89) correspond to those in Tgo-Pol (shown in panel B) which form the pocket. Both V8 and Q10 are near the position of the Tgo-Pol Y7. α-Helices are shown (24) and β-sheets (25). Images/structural homology models were produced using Swiss-Model [N. Guex, M. C. Peitsch, *Electrophoresis* 18, 2714 (1997)] (http://www.expasy.ch/spdbv/), POV-Ray [C. Cason, POV-Ray for Windows, version 3.1g (1999)] (http://www.povray.org) and Rasmol [R. Sayle, J. F. Milner-White, *Trends Biochem. Sci.* 20, 374 (1995)].

At page 17, in the paragraph following "Example 1" please amend the journal name for the Hopfner et al citation as follows:

Crystal structures are known for five family B DNA polymerases; one viral, the remaining four archaeal. The first structure to be solved was for the bacteriophage RB69 polymerase (RB69-Pol) (J. Wang *et al., Cell* 89, 1087 (1997)); a structure with primer-template has also been determined (M. C. Franklin, J. J. Wang, T. A. Steitz, *Cell* 105, 657 (2001)). More recently, the structure of an archaeal family B DNA polymerase, from the hyperthermophilic archaeon *Thermococcus gorgonarius* (Tgo-Pol), has been reported (K. P. Hopfner *et al.*, Structure 7, 1189 PNAS 96, 3600 (1999)). Three other archaeal polymerase structures, *Desulfurococcus* strain Tok (DTok-Pol) (Y. Zhao *et al.*, *Structure* 7, 1189 (1999)). Three other archaeal polymerase structures, *Desulfurococcus* strain Tok (DTok-Pol) (Y. Zhao *et al.*, *Structure* 7, 1189 (1999)), *Thermococcus sp.* 9°N-7 (9°N-7-Pol) (A. C. Rodgriguez, H-W. Park,

C. Mao, L. S. Beese, *J. Mol. Biol.* **299**, 447 (200)) and *Pyrococcus kodakaraensis* KOD1 (KOD1-Pol) (H. Hashimoto *et al.*, *J. Mol. Biol.* **306**, 469 (2001)), were subsequently solved. Only apo-enzyme structures are known for the archaea. All five family B polymerases contain five distinct domains, the N-terminal domain, the exonuclease or 'editing' domain and three polymerase active site domains. The folding of the five domains forms three distinct clefts extending from a central hole. Two (named clefts D and T) are oriented approximately 180° relative to each other, on either side of the central hole. The structure of RB69-pol containing a primer-template demonstrates that cleft D binds double stranded primer-template and cleft T binds single-stranded template (M. C. Franklin *et al supra*). The three polymerase domains forms cleft D, whereas cleft T is formed by the exonuclease domain and the N-terminal domain. The third cleft is perpendicular to the other two and represents the 3'-5' exonuclease/editing cleft.